

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 15, 2001, 10:36:11 ; Search time 30.06 Seconds
(without alignments)
11.294 Million cell updates/sec

Title: US-09-288-719-1

Perfect score: 28

Sequence: 1 GGGGS 5

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR66:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	28	100.0	37	2	S29113	diptericin homolog
2	28	100.0	69	1	MIEC77	microcin B17 precu
3	28	100.0	80	2	T10550	hypothetical prote
4	28	100.0	81	2	PC2047	grain-softness pro
5	28	100.0	82	2	S19774	glycine-rich prote
6	28	100.0	85	2	T32664	hypothetical prote
7	28	100.0	92	2	P00743	grain-softness pro
8	28	100.0	97	2	T46330	hypothetical prote
9	28	100.0	100	2	T49621	hypothetical prote
10	28	100.0	102	2	T25332	hypothetical prote
11	28	100.0	104	2	T02612	hypothetical prote
12	28	100.0	104	2	UC4190	hypothetical prote
13	28	100.0	109	2	S58673	holotricin 3 precu
14	28	100.0	114	2	S28821	RNA-binding protei
15	28	100.0	115	2	T35387	transcription fact
16	28	100.0	119	2	T07695	hypothetical prote
17	28	100.0	120	2	A81109	hypothetical prote
18	28	100.0	120	2	D83415	hypothetical prote
19	28	100.0	122	2	T04118	mitochondrial proc
20	28	100.0	125	2	T16247	hypothetical prote
21	28	100.0	128	2	T30428	hypothetical prote
22	28	100.0	129	2	A33976	NK-1 homeotic prot
23	28	100.0	131	2	H69062	molybdenum transpo
24	28	100.0	133	2	G75432	hypothetical prote
25	28	100.0	135	2	S55647	hypothetical prote
26	28	100.0	136	2	T02870	globulin 2 precurs
27	28	100.0	136	2	T29282	hypothetical prote
28	28	100.0	144	2	S04069	glycine-rich prote
29	28	100.0	144	2	S35716	glycine-rich prote

30	28	100.0	144	2	T34730	probable gas vesic
31	28	100.0	145	1	J01062	glycine-rich prote
32	28	100.0	148	2	S46514	puroindoline-b pre
33	28	100.0	148	2	I38881	caudal-type homeot
34	28	100.0	149	2	T23179	hypothetical prote
35	28	100.0	152	2	T04811	STIG1 protein homo
36	28	100.0	155	2	T51842	RING-H2 finger pro
37	28	100.0	157	1	S14857	glycine-rich prote
38	28	100.0	165	1	KNR2G1	glycine-rich cell
39	28	100.0	167	2	S21359	keratin, type I, c
40	28	100.0	168	2	T50922	bZIP protein HY5 f
41	28	100.0	169	2	T51586	hypothetical prote
42	28	100.0	169	2	T47558	hypothetical prote
43	28	100.0	173	2	J01064	glycine-rich prote
44	28	100.0	173	2	A47303	FT2-F1 steroid rec
45	28	100.0	174	2	S68274	inositol 1,4,5-tri

ALIGNMENTS

RESULT 1
S29113
diptericin homolog - flesh fly (*Sarcophaga peregrina*)
C:Species: *Sarcophaga peregrina*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S29113
R: Ishikawa, M.; Kubo, T.; Natori, S.
Biochem. J. 287, 573-578, 1992
A:Title: Purification and characterization of a diptericin homologue from *Sarcophaga*
A:Reference number: S29113; M0ID:93074966
A:Accession: S29113
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-37 <ISH>

Query Match 100.0%; Score 28; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
DB 19 GGGGS 23

RESULT 2
MIEC77
microcin B17 precursor - *Escherichia coli* plasmid pMCB17
C:Species: *Escherichia coli*
C:Date: 30-Jun-1988 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C:Accession: A25219; A32058; I41099; A58368; S67977
R: Davagnano, J.; Herrero, M.; Furlong, D.; Moreno, F.; Kolter, R.
Proteins 1, 230-238, 1986
A:Title: The DNA replication inhibitor microcin B17 is a forty-three-amino-acid prote
A:Reference number: A25219; M0ID:88217867
A:Accession: A25219
A:Molecule type: DNA
A:Residues: 1-69 <DNA>
A:Cross-references: GB:M15469; NID:q146787; PIDN:AAA24141.1; PID:q146788
R:geniloud, O.; Moreno, F.; Kolter, R.
J. Bacteriol. 171, 1126-1135, 1989
A:Title: DNA sequence, products, and transcriptional pattern of the genes involved in
A:Reference number: A32058; M0ID:89123111
A:Accession: A32058
A:Molecule type: DNA
A:Residues: 1-69 <GEN>
A:Cross-references: GB:M24253; NID:q341145; PIDN:AAA72741.1; PID:q522290
R:Connell, N.; Han, Z.; Moreno, F.; Kolter, R.
Mol. Microbiol. 1, 195-201, 1987
A:Title: An *E. coli* promoter induced by the cessation of growth.
A:Reference number: I41099; M0ID:88216163
A:Accession: I41099

A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-14 <CON>
A:Cross-references: EMBL:X06417; NID:g41978; PIDN:CAA29725.1; PID:g41979
R.Li, Y.M.; Milne, J.C.; Madison, L.L.; Kolter, R.; Walsh, C.T.
Science 274, 1188-1193, 1996
A:Title: From peptide precursors to oxazole and thiazole-containing peptide antibiotics:
A:Reference number: A58368; MUID:97053605
A:Accession: A58368
A:Molecule type: protein
A:Residues: 27-38 <LIV>
A:Experimental source: Escherichia coli strain ZK4(PY113)
A:Note: mass spectroscopy of peptides and biosynthetic intermediates
R.Yorgey, P.; Lee, J.; Koedel, J.; Vivas, E.; Warner, P.; Jedartnam, D.; Kolter, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
A:Title: Posttranslational modifications in microcin B17 define an additional class of D
A:Reference number: A58375; MUID:94240167
A:Contents: annotation: (1)H-NMR spectroscopy of modified peptides
R.Bayer, A.; Freund, S.; Jung, G.
Eur. J. Biochem. 234, 414-426, 1995
A:Title: Post-translational heterocyclic backbone modifications in the 43-peptide antibi
A:Reference number: S67977; MUID:96128168
A:Accession: S67977
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-38 <BAY>
A:Genetics:
A:Gene: mcba
A:Genome: plasmid pmcCB17
C:Function:
A:Description: inhibits DNA gyrase, stopping DNA replication
A:Note: active against a large number of gram-negative enteric bacteria
C:Superfamily: microcin
C:Keywords: antibiotic; DNA replication inhibitor; oxazole/thiazole ring
F:1-26/Domain: signal sequence #status predicted <STG>
F:27-69/Product: microcin B17 #status experimental <MAT>
F:39-40/Cross-link: oxazole (Gly-Ser) #status experimental
F:40-41/Cross-link: thiazole (Ser-Cys) #status experimental
F:47-48/Cross-link: thiazole (Gly-Cys) #status experimental
F:50-51/Cross-link: thiazole (Gly-Cys) #status experimental
F:54-55/Cross-link: thiazole (Gly-Cys) #status experimental
F:55-56/Cross-link: oxazole (Cys-Ser) #status experimental
F:61-62/Cross-link: oxazole (Gly-Ser) #status experimental
F:64-65/Cross-link: oxazole (Gly-Ser) #status experimental

Query Match 100.0%; Score 28; DB 1; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
Db 36 GGGGS 40

RESULT 3
T10550
hypothetical protein T12G13.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C:Accession: T10550
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16533
A:Accession: T10550
A:Molecule type: DNA
A:Residues: 1-80 <BEV>
A:Cross-references: EMBL:AL080252; GSPDB:GN00062; ATSP:T12G13.70
A:Experimental source: cultivar Columbia; BAC clone T12G13
C:Genetics:
A:Gene: ATSP:T12G13.70
A:Map position: 4
A:Status: preliminary; translated from GB/EMBL/DBD

Query Match 100.0%; Score 28; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
Db 27 GGGGS 31

RESULT 4
PC2047
grain-softness protein - wheat (fragments)
C:Species: Triticum aestivum (common wheat)
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 14-Sep-1994
C:Accession: PC2047
R.Jolly, C.J.; Rahman, S.; Kortt, A.A.; Higgins, T.J.V.
Theor. Appl. Genet. 86, 589-597, 1993
A:Title: Characterisation of the wheat Mr 15000 grain-softness protein and analysis o
A:Reference number: PQ0743
A:Accession: PC2047
A:Molecule type: protein
A:Residues: 1-18;19-24;25-31;32-38;39-45;46-51;52-56;57-60;61-65;66-71;72-77;78-81 <J
C:Comment: This protein is the product of the Ha locus and thus be the major factor t
C:Keywords: seed

Query Match 100.0%; Score 28; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
Db 4 GGGGS 8

RESULT 5
S19774
glycine-rich protein - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C:Accession: S19774
R:Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A:Reference number: S19774
A:Accession: S19774
A:Molecule type: mRNA
A:Residues: 1-82 <PAR>
A:Cross-references: EMBL:X59883; NID:g19321; PIDN:CAA42538.1; PID:g19322
C:Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology

Query Match 100.0%; Score 28; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
Db 72 GGGGS 76

RESULT 6
T13664
hypothetical protein F16B4.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Jun-2000
C:Accession: T13664
R:Davidson, S.; Wohlmann, P.; Bauer, C.; O'Neal, D.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid F16B4.
A:Reference number: Z21208
A:Accession: T13664
A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA
 A:Residues: 1-85 <DAV>
 A:Cross-references: EMBL:AF039048; PIDN:AA94238.1; GSPDB:GN00023; CESP:F16B4.7
 A:Experimental source: strain Bristol N2; clone F16B4
 C:Genetics:
 A:Gene: CESP:F16B4.7
 A:Map position: 5
 A:Introns: 36/1
 C:Superfamily: Arabidopsis glycine-rich protein 3

Query Match 100.0%; Score 28; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 |||||
 Db 39 GGGGS 43

RESULT 7
 P00743

grain-softness protein - wheat (fragments)
 C:Species: Triticum aestivum (common wheat)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 23-Mar-1995
 C:Accession: P00743
 R:Jolly, C.J.; Rahman, S.; Kortt, A.A.; Higgins, T.J.V.
 Theor. Appl. Genet. 86, 589-597, 1993
 A:Title: Characterisation of the wheat Mr 15000 grain-softness protein and analysis of
 A:Reference number: P00743
 A:Accession: P00743
 A:Molecule type: protein
 A:Residues: 1-92 <JOL>
 A:Experimental source: seed
 C:Keywords: seed

Query Match 100.0%; Score 28; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 |||||
 Db 4 GGGGS 8

RESULT 8
 T48330

hypothetical protein F15A17.120 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48330
 R:Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De
 ewes, H.W.; Rudd, S.; Lemcke, K.; Meyer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24491
 A:Accession: T48330
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-97 <BEV>
 A:Cross-references: EMBL:AL163002
 A:Experimental source: cultivar Columbia; BAC clone F15A17
 C:Genetics:
 A:Map position: 5
 A:Introns: 7/1
 A:Note: F15A17.120

Query Match 100.0%; Score 28; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5

Db 47 GGGGS 51
 |||||

RESULT 9
 T49621

hypothetical protein B5022.30 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49621
 R:Schulte, U.; Aign, V.; Hohnsels, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
 submitted to the Protein Sequence Database, May 2000
 A:Reference number: Z25022
 A:Accession: T49621
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-100 <SCH>
 A:Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.30
 A:Experimental source: BAC clone B5022; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B5022.30
 A:Map position: 6
 A:Introns: 22/1; 52/1

Query Match 100.0%; Score 28; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 |||||
 Db 11 GGGGS 15

RESULT 10
 T25332

hypothetical protein T26H5.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T25332
 R:Gardner, A.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z20017
 A:Accession: T25332
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-102 <WIL>
 A:Cross-references: EMBL:T28056; PIDN:CAB04855.1; GSPDB:GN00023; CESP:T26H5.4
 A:Experimental source: clone T26H5
 C:Genetics:
 A:Gene: CESP:T26H5.4
 A:Map position: 5
 A:Introns: 13/1; 96/1
 C:Superfamily: hypothetical protein K01D12.8

Query Match 100.0%; Score 28; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGGS 5
 |||||
 Db 52 GGGGS 56

RESULT 11
 T02612

hypothetical protein T19L18.7 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 14-May-1999
 C:Accession: T02612
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
 submitted to the EMBL Data Library, August 1998

A:Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A:Reference number: 214681
A:Accession: T02612
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-104 <R0U>
A:Cross-references: EMBL:AC004747; NID:g3413696; PID:g3413702
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 2
A:Introns: 49/3
A:Note: T19L18.7

Query Match 100.0%; Score 28; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
DB 96 GGGGS 100

RESULT 12

JC4190
holotrichin 3 precursor - Holotrichia diomphalia
N:Alternate names: antifungal protein
C:Species: Holotrichia diomphalia
C:Date: 04-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: JC4190
R:Lee, S.Y.; Moon, H.J.; Kurata, S.; Natori, S.; Lee, B.L.
Biol. Pharm. Bull. 18, 1049-1052, 1995
A:Title: Purification and cDNA cloning of an antifungal protein from the hemolymph of H.
A:Reference number: JC4190; MUID:96073722
A:Accession: JC4190
A:Molecule type: mRNA
A:Residues: 1-104 <LEE>
A:Cross-references: DDBJ:D13744; NID:g1088433; PIDN:BA02889.1; PID:d1003394; PID:g17861
C:Comment: This protein is a Gly- and His-rich protein and a constitutive protein of Iar
C:Keywords: hemolymph signal sequence #status predicted <SIG>
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-104/Product: holotrichin 3 #status predicted <MAT>

Query Match 100.0%; Score 28; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
DB 69 GGGGS 73

RESULT 13

SS8673
RNA-binding protein Rbpc - Anabaena variabilis (fragment)
C:Species: Anabaena variabilis
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 28-May-1999
C:Accession: SS8673
R:Sato, N.
Nucleic Acids Res. 23, 2161-2167, 1995
A:Title: A family of cold-regulated RNA-binding protein genes in the cyanobacterium Anab
A:Reference number: SS8673; MUID:95334368
A:Accession: SS8673
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-109 <SAT>
A:Cross-references: GB:D49424; NID:g1064776; PIDN:BA08402.1; PID:d1008998; PID:g1064777
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein
F:1-68/Domain: ribonucleoprotein repeat homology <RM2>

Query Match 100.0%; Score 28; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
DB 88 GGGGS 92

RESULT 14

S28821
transcription factor ets-988 - fruit fly (Drosophila melanogaster) (fragment)
N:Alternate names: transforming protein ets-4
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000
C:Accession: S28821
R:Chen, T.; Bunting, M.; Karim, F.D.; Thummel, C.S.
Dev. Biol. 151, 176-191, 1992
A:Title: Isolation and characterization of five Drosophila genes that encode an ets-r
A:Reference number: S28819; MUID:92249640
A:Accession: S28821
A:Molecule type: DNA
A:Residues: 1-114 <CHE>
A:Cross-references: EMBL:M88474; NID:g157195; PIDN:AAA28451.1; PID:g157196
C:Genetics:
A:Gene: Ets988
A:Cross-references: FlyBase:FBgn0005659
C:Superfamily: ets DNA-binding domain homology
C:Keywords: DNA binding; nucleus; transcription factor
F:28-109/Domain: ets DNA-binding domain homology <ETS>

Query Match 100.0%; Score 28; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
DB 20 GGGGS 24

RESULT 15

T35387
hypothetical protein SC6673.30C - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T35387
R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21576
A:Accession: T35387
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-115 <MUR>
A:Cross-references: EMBL:AL079348; PIDN:CAB45486.1; GSPDB:GN00070; SCOEDB:SC6673.30C
C:Experimental source: strain A3(2)
A:Gene: SCOEDB:SC6673.30C
C:Superfamily: Escherichia coli ybab protein

Query Match 100.0%; Score 28; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGS 5
|||||
DB 104 GGGGS 108

Search completed: March 15, 2001, 10:52:55
Job time: 1004 sec
